

OIPE

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/10/021,753

TIME: 19:11:23

Input Set : A:\UTSH251US.txt

Output Set: N:\CRF3\01152002\J021753.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: FUJISE, KEN
 4 YEH, EDWARD T.H.
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO FORTILIN, AN
 7 ANTI-APOPTOTIC MOLECULE, AND MODULATORS OF FORTILIN
 9 <130> FILE REFERENCE: UTSH:251US
 11 <140> CURRENT APPLICATION NUMBER: US/10/021,753
 12 <141> CURRENT FILING DATE: 2001-10-30
 14 <140> CURRENT APPLICATION NUMBER: 60/244,416
 15 <141> CURRENT FILING DATE: 2000-10-30
 17 <160> NUMBER OF SEQ ID NOS: 9
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 830
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (95)..(613)
 30 <400> SEQUENCE: 1
 31 cccccccgag cgccgctccg gctgcaccgc gctcgctccg agtttcaggc tcgtgctaag 60
 33 ctacgcgcgt cgctgctctcc cttcagtcgc catc atg att atc tac cgg gac ctc 115
 34 Met Ile Ile Tyr Arg Asp Leu
 35 1 5
 37 atc agc cac gat gag atg ttc tcc gac atc tac aag atc cgg gag atc 163
 38 Ile Ser His Asp Glu Met Phe Ser Asp Ile Tyr Lys Ile Arg Glu Ile
 39 10 15 20
 41 gcg gac ggg ttg tgc ctg gag gtg gag ggg aag atg gtc agt agg aca 211
 42 Ala Asp Gly Leu Cys Leu Glu Gly Lys Met Val Ser Arg Thr
 43 25 30 35
 45 gaa ggt aac att gat gac tcg ctc att ggt gga aat gcc tcc gct gaa 259
 46 Glu Gly Asn Ile Asp Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu
 47 40 45 50 55
 49 ggc ccc gag ggc gaa ggt acc gaa agc aca gta atc act ggt gtc gat 307
 50 Gly Pro Glu Gly Glu Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp
 51 60 65 70
 53 att gtc atg aac cat cac ctg cag gaa aca agt ttc aca aaa gaa gcc 355
 54 Ile Val Met Asn His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala
 55 75 80 85
 57 tac aag aag tac atc aaa gat tac atg aaa tca atc aaa ggg aaa ctt 403
 58 Tyr Lys Lys Tyr Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu
 59 90 95 100
 61 gaa gaa cag aga cca gaa aga gta aaa cct ttt atg aca ggg gct gca 451
 62 Glu Glu Gln Arg Pro Glu Arg Val Lys Pro Phe Met Thr Gly Ala Ala
 63 105 110 115
 65 gaa caa atc aag cac atc ctt gct aat ttc aaa aac tac cag ttc ttt 499
 66 Glu Gln Ile Lys His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Phe Phe
 67 120 125 130 135

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69 att ggt gaa aac atg aat cca gat ggc atg gtt gct cta ttg gac tac 547
70 Ile Gly Glu Asn Met Asn Pro Asp Gly Met Val Ala Leu Leu Asp Tyr
71      140      145      150
73 cgt gag gat ggt gtg acc cca tat atg att ttc ttt aag gat ggt tta 595
74 Arg Glu Asp Gly Val Thr Pro Tyr Met Ile Phe Phe Lys Asp Gly Leu
75      155      160      165
77 gaa atg gaa aaa tgt taa caaatgtggc aattattttg gatctatcac 643
78 Glu Met Glu Lys Cys
79      170
81 ctgtcatcat aactggcttc tgcttgtcat ccacacaaca ccaggactta agacaaatgg 703
83 gactgatgtc atcttgagct cttcatttat tttgactgtg atttatttgg agtggaggca 763
85 ttgttttttaa gaaaaacatg tcatgtaggt tgtctaaaaa taaaatgcat ttaaaactcat 823
87 ttgagag 830
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 172
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
95 <400> SEQUENCE: 2
96 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
97 1 5 10 15
98 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
99 20 25 30
100 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
101 35 40 45
102 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
103 50 55 60
104 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
105 65 70 75 80
106 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
107 85 90 95
108 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
109 100 105 110
110 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
111 115 120 125
112 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
113 130 135 140
114 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
115 145 150 155 160
116 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
117 165 170
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 172
123 <212> TYPE: PRT
124 <213> ORGANISM: Rabbit
126 <400> SEQUENCE: 3
127 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
128 1 5 10 15
130 Ile Tyr Lys Ile Arg Glu Ile Ala Gly Gly Leu Cys Leu Glu Val Glu
131 20 25 30

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133 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
134           35           40           45
136 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
137           50           55           60
139 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
140 65           70           75           80
142 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
143           85           90           95
145 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
146           100          105          110
148 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
149           115          120          125
151 Phe Lys Asn Tyr Gln Phe Tyr Ile Gly Glu Asn Met Asn Pro Asp Gly
152 130          135          140
154 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
155 145          150          155          160
157 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
158           165          170

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161 <210> SEQ ID NO: 4

162 <211> LENGTH: 172

163 <212> TYPE: PRT

164 <213> ORGANISM: Mus musculus

166 <400> SEQUENCE: 4

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167 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Leu Phe Ser Asp
168 1           5           10           15
170 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
171           20           25           30
173 Gly Lys Met Val Ser Arg Thr Glu Gly Ala Ile Asp Asp Ser Leu Ile
174           35           40           45
176 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
177           50           55           60
179 Thr Val Val Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
180 65           70           75           80
182 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
183           85           90           95
185 Lys Ser Leu Lys Gly Lys Leu Glu Glu Gln Lys Pro Glu Arg Val Lys
186           100          105          110
188 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
189           115          120          125
191 Phe Asn Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
192 130          135          140
194 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
195 145          150          155          160
197 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
198           165          170

```

201 <210> SEQ ID NO: 5

202 <211> LENGTH: 172

203 <212> TYPE: PRT

204 <213> ORGANISM: Chicken

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206 <400> SEQUENCE: 5
207 Met Ile Ile Tyr Arg Asp Cys Ile Ser Gln Asp Glu Met Phe Ser Asp
208 1 5 10 15
210 Ile Tyr Lys Ile Arg Glu Val Ala Asn Gly Leu Cys Leu Glu Val Glu
211 20 25 30
213 Gly Lys Met Val Thr Arg Thr Glu Gly Gln Ile Asp Asp Ser Leu Ile
214 35 40 45
216 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ala
217 50 55 60
219 Thr Val Ile Thr Gly Val Asp Ile Val Ile Asn His His Leu Gln Glu
220 65 70 75 80
222 Thr Ser Phe Thr Lys Glu Ser Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
223 85 90 95
225 Lys Ala Ile Lys Ala Arg Leu Glu Glu His Lys Pro Glu Arg Val Lys
226 100 105 110
228 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
229 115 120 125
231 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
232 130 135 140
234 Met Val Ala Leu Leu Asp Phe Arg Glu Asp Gly Val Thr Pro Tyr Met
235 145 150 155 160
237 Ile Phe Phe Lys Asp Gly Leu Glu Ile Glu Lys Cys
238 165 170
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 172
243 <212> TYPE: PRT
244 <213> ORGANISM: D. Melanogaster
246 <400> SEQUENCE: 6
247 Met Lys Ile Tyr Lys Asp Ile Ile Thr Gly Asp Glu Met Phe Ala Asp
248 1 5 10 15
250 Thr Tyr Lys Met Lys Leu Val Asp Asp Val Ile Tyr Glu Val Tyr Gly
251 20 25 30
253 Lys Leu Ile Thr Arg Gln Gly Asp Asp Ile Lys Leu Glu Gly Ala Asn
254 35 40 45
256 Ala Ser Ala Glu Glu Ala Asp Glu Gly Thr Asp Ile Thr Ser Glu Ser
257 50 55 60
259 Gly Val Asp Val Val Leu Asn His Arg Leu Thr Glu Cys Phe Ala Phe
260 65 70 75 80
262 Gly Asp Lys Lys Ser Tyr Thr Leu Tyr Leu Lys Asp Tyr Met Lys Lys
263 85 90 95
265 Val Leu Ala Lys Leu Glu Glu Lys Ser Pro Asp Gln Val Asp Ile Phe
266 100 105 110
268 Lys Thr Asn Met Asn Lys Ala Met Lys Asp Ile Leu Gly Arg Phe Lys
269 115 120 125
271 Glu Leu Gln Phe Phe Thr Gly Glu Ser Met Asp Cys Asp Gly Met Val
272 130 135 140
274 Ala Leu Val Glu Tyr Arg Glu Ile Asn Gly Asp Ser Val Pro Val Leu
275 145 150 155 160
277 Met Phe Phe Lys His Gly Leu Glu Glu Glu Lys Cys

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278                               165                               170
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 181
283 <212> TYPE: PRT
284 <213> ORGANISM: C. ELEGANS
286 <400> SEQUENCE: 7
287 Met Leu Ile Tyr Lys Asp Ile Ile Ser Asp Asp Glu Leu Ser Ser Asp
288   1                               5                               10                               15
290 Ser Phe Pro Met Lys Leu Val Asp Asp Leu Val Tyr Glu Phe Lys Gly
291                               20                               25                               30
293 Lys His Val Val Arg Lys Glu Gly Glu Ile Val Leu Ala Gly Ser Asn
294                               35                               40                               45
296 Pro Ser Ala Glu Glu Gly Ala Glu Asp Asp Gly Ser Asp Glu His Val
297   50                               55                               60
299 Glu Arg Gly Ile Asp Ile Val Leu Asn His Lys Leu Val Glu Met Asn
300  65                               70                               75                               80
302 Cys Tyr Glu Asp Ala Ser Met Phe Lys Ala Tyr Ile Lys Lys Phe Met
303                               85                               90                               95
305 Lys Asn Val Ile Asp His Met Glu Lys Asn Asn Arg Asp Lys Ala Asp
306                               100                              105                              110
308 Val Asp Ala Phe Lys Lys Lys Ile Gln Gly Trp Val Val Ser Leu Leu
309                               115                              120                              125
311 Ala Lys Asp Arg Phe Lys Asn Leu Ala Phe Phe Ile Gly Glu Arg Ala
312  130                              135                              140
314 Ala Glu Gly Ala Glu Asn Gly Gln Val Ala Ile Ile Glu Tyr Arg Asp
315 145                              150                              155                              160
317 Val Asp Gly Thr Glu Val Pro Thr Leu Met Leu Val Lys Glu Ala Ile
318                               165                               170                               175
320 Ile Glu Glu Lys Cys
321                               180
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 166
326 <212> TYPE: PRT
327 <213> ORGANISM: S. Cerevisiae
329 <400> SEQUENCE: 8
330 Met Ile Ile Tyr Lys Asp Ile Phe Ser Asn Asp Glu Leu Leu Ser Asp
331   1                               5                               10                               15
333 Ala Tyr Asp Ala Lys Leu Val Asp Asp Val Ile Tyr Glu Ala Asp Cys
334                               20                               25                               30
336 Ala Met Val Asn Val Gly Gly Asp Asn Ile Asp Ile Gly Ala Asn Pro
337                               35                               40                               45
339 Ser Ala Glu Gly Gly Asp Asp Asp Val Glu Glu Gly Ala Glu Met Val
340   50                               55                               60
342 Asn Asn Val Val His Ser Phe Arg Leu Gln Gln Thr Ala Phe Asp Lys
343  65                               70                               75                               80
345 Lys Ser Phe Leu Thr Tyr Ile Lys Gly Tyr Met Lys Ala Val Lys Ala
346                               85                               90                               95
348 Lys Leu Gln Glu Thr Asn Pro Glu Glu Val Pro Lys Phe Glu Lys Gly
349                               100                              105                              110

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VERIFICATION SUMMARY

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Input Set : A:\UTSH251US.txt

Output Set: N:\CRF3\01152002\J021753.raw

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L:14 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:14 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date